

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/562,132
Source: IFWP
Date Processed by STIC: 3/6/07

ENTERED



IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/562,132

DATE: 03/06/2007
TIME: 08:51:32

Input Set : A:\126446.ST25.txt
Output Set: N:\CRF4\03062007\J562132.raw

3 <110> APPLICANT: Pedersen, Susanne
 4 Cole, Robert
 5 Wienberger, Ron
 6 Sloane, Andrew
 8 <120> TITLE OF INVENTION: Method of isolating a protein
 10 <130> FILE REFERENCE: FBR0005-100
 12 <140> CURRENT APPLICATION NUMBER: 10/562,132
 C--> 14 <141> CURRENT FILING DATE: 2005-12-23
 14 <150> PRIOR APPLICATION NUMBER: AU 2003903317
 15 <151> PRIOR FILING DATE: 2003-06-27
 17 <150> PRIOR APPLICATION NUMBER: PCT/AU2004/00856
 18 <151> PRIOR FILING DATE: 2004-06-28
 20 <160> NUMBER OF SEQ ID NOS: 26
 22 <170> SOFTWARE: PatentIn version 3.3
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 593
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Streptococcus sp.
 29 <400> SEQUENCE: 1
 31 Met Glu Lys Glu Lys Lys Val Lys Tyr Phe Leu Arg Lys Ser Ala Phe
 32 1 5 10 15
 35 Gly Leu Ala Ser Val Ser Ala Ala Phe Leu Val Gly Ser Thr Val Phe
 36 20 25 30
 39 Ala Val Asp Ser Pro Ile Glu Asp Thr Pro Ile Ile Arg Asn Gly Gly
 40 35 40 45
 43 Glu Leu Thr Asn Leu Leu Gly Asn Ser Glu Thr Thr Leu Ala Leu Arg
 44 50 55 60
 47 Asn Glu Glu Ser Ala Thr Ala Asp Leu Thr Ala Ala Ala Val Ala Asp
 48 65 70 75 80
 51 Thr Val Ala Ala Ala Ala Glu Asn Ala Gly Ala Ala Ala Trp Glu
 52 85 90 95
 55 Ala Ala Ala Ala Asp Ala Leu Ala Lys Ala Lys Ala Asp Ala Leu
 56 100 105 110
 59 Lys Glu Phe Asn Lys Tyr Gly Val Ser Asp Tyr Tyr Lys Asn Leu Ile
 60 115 120 125
 63 Asn Asn Ala Lys Thr Val Glu Gly Val Lys Asp Leu Gln Ala Gln Val
 64 130 135 140
 67 Val Glu Ser Ala Lys Lys Ala Arg Ile Ser Glu Ala Thr Asp Gly Leu
 68 145 150 155 160
 71 Ser Asp Phe Leu Lys Ser Gln Thr Pro Ala Glu Asp Thr Val Lys Ser
 72 165 170 175
 75 Ile Glu Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys
 76 180 185 190

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79 Tyr Gly Val Ser Asp Tyr His Lys Asn Leu Ile Asn Asn Ala Lys Thr
 80 195 200 205
 83 Val Glu Gly Val Lys Asp Leu Gln Ala Gln Val Val Glu Ser Ala Lys
 84 210 215 220
 87 Lys Ala Arg Ile Ser Glu Ala Thr Asp Gly Leu Ser Asp Phe Leu Lys
 88 225 230 235 240
 91 Ser Gln Thr Pro Ala Glu Asp Thr Val Lys Ser Ile Glu Leu Ala Glu
 92 245 250 255
 95 Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly Val Ser Asp
 96 260 265 270
 99 Tyr Tyr Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu Gly Val Lys
 100 275 280 285
 103 Ala Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro Lys Thr Asp Thr Tyr
 104 290 295 300
 107 Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Glu
 108 305 310 315 320
 111 Ala Val Asp Ala Ala Thr Ala Glu Lys Val Phe Lys Gln Tyr Ala Asn
 112 325 330 335
 115 Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr Asp Asp Ala Thr Lys Thr
 116 340 345 350
 119 Phe Thr Val Thr Glu Lys Pro Glu Val Ile Asp Ala Ser Glu Leu Thr
 120 355 360 365
 123 Pro Ala Val Thr Tyr Lys Leu Val Ile Asn Gly Lys Thr Leu Lys
 124 370 375 380
 127 Gly Glu Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val
 128 385 390 395 400
 131 Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr
 132 405 410 415
 135 Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile
 136 420 425 430
 139 Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile
 140 435 440 445
 143 Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Thr Lys Ala Val Asp Ala
 144 450 455 460
 147 Glu Thr Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val
 148 465 470 475 480
 151 Asp Gly Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr
 152 485 490 495
 155 Glu Met Val Thr Glu Val Pro Gly Asp Ala Pro Thr Glu Pro Glu Lys
 156 500 505 510
 159 Pro Glu Ala Ser Ile Pro Leu Val Pro Leu Thr Pro Ala Thr Pro Ile
 160 515 520 525
 163 Ala Lys Asp Asp Ala Lys Lys Asp Asp Thr Lys Lys Glu Asp Ala Lys
 164 530 535 540
 167 Lys Pro Glu Ala Lys Lys Glu Asp Ala Lys Lys Ala Glu Thr Leu Pro
 168 545 550 555 560
 171 Thr Thr Gly Glu Gly Ser Asn Pro Phe Phe Thr Ala Ala Ala Leu Ala
 172 565 570 575
 175 Val Met Ala Gly Ala Gly Ala Leu Ala Val Ala Ser Lys Arg Lys Glu

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| | | | |
|---|-----|-----|-----|
| 176 | 580 | 585 | 590 |
| 179 Asp | | | |
| 183 <210> SEQ ID NO: 2 | | | |
| 184 <211> LENGTH: 454 | | | |
| 185 <212> TYPE: PRT | | | |
| 186 <213> ORGANISM: Staphylococcus aureus | | | |
| 188 <400> SEQUENCE: 2 | | | |
| 190 Met Met Thr Leu Gln Ile His Thr Gly Gly Ile Asn Leu Lys Lys Lys | | | |
| 191 1 5 10 15 | | | |
| 194 Asn Ile Tyr Ser Ile Arg Lys Leu Gly Val Gly Ile Ala Ser Val Thr | | | |
| 195 20 25 30 | | | |
| 198 Leu Gly Thr Leu Leu Ile Ser Gly Gly Val Thr Pro Ala Ala Asn Ala | | | |
| 199 35 40 45 | | | |
| 202 Ala Gln His Asp Glu Ala Gln Gln Asn Ala Phe Tyr Gln Val Leu Asn | | | |
| 203 50 55 60 | | | |
| 206 Met Pro Asn Leu Asn Ala Asp Gln Arg Asn Gly Phe Ile Gln Ser Leu | | | |
| 207 65 70 75 80 | | | |
| 210 Lys Asp Asp Pro Ser Gln Ser Ala Asn Val Leu Gly Glu Ala Gln Lys | | | |
| 211 85 90 95 | | | |
| 214 Leu Asn Asp Ser Gln Ala Pro Lys Ala Asp Ala Gln Gln Asn Lys Phe | | | |
| 215 100 105 110 | | | |
| 218 Asn Lys Asp Gln Gln Ser Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn | | | |
| 219 115 120 125 | | | |
| 222 Leu Asn Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp | | | |
| 223 130 135 140 | | | |
| 226 Pro Ser Gln Ser Thr Asn Val Leu Gly Glu Ala Lys Lys Leu Asn Glu | | | |
| 227 145 150 155 160 | | | |
| 230 Ser Gln Ala Pro Lys Ala Asp Asn Asn Phe Asn Lys Glu Gln Gln Asn | | | |
| 231 165 170 175 | | | |
| 234 Ala Phe Tyr Glu Ile Leu Asn Met Pro Asn Leu Asn Glu Glu Gln Arg | | | |
| 235 180 185 190 | | | |
| 238 Asn Gly Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn | | | |
| 239 195 200 205 | | | |
| 242 Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Ala | | | |
| 243 210 215 220 | | | |
| 246 Asp Asn Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu | | | |
| 247 225 230 235 240 | | | |
| 250 His Leu Pro Asn Leu Thr Glu Glu Gln Arg Asn Gly Phe Ile Gln Ser | | | |
| 251 245 250 255 | | | |
| 254 Leu Lys Asp Asp Pro Ser Val Ser Lys Glu Ile Leu Ala Glu Ala Lys | | | |
| 255 260 265 270 | | | |
| 258 Lys Leu Asn Asp Ala Gln Ala Pro Lys Glu Glu Asp Asn Asn Lys Pro | | | |
| 259 275 280 285 | | | |
| 262 Gly Lys Glu Asp Asn Asn Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro | | | |
| 263 290 295 300 | | | |
| 266 Gly Lys Glu Asp Asn Lys Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro | | | |
| 267 305 310 315 320 | | | |
| 270 Gly Lys Glu Asp Asn Lys Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro | | | |
| 271 325 330 335 | | | |

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274 Gly Lys Glu Asp Gly Asn Lys Pro Gly Lys Glu Asp Gly Asn Lys Pro
 275 340 345 350
 278 Gly Lys Glu Asp Gly Asn Gly Val His Val Val Lys Pro Gly Asp Thr
 279 355 360 365
 282 Val Asn Asp Ile Ala Lys Ala Asn Gly Thr Thr Ala Asp Lys Ile Ala
 283 370 375 380
 286 Val Asp Asn Lys Leu Ala Asp Lys Asn Met Ile Lys Pro Gly Gln Glu
 287 385 390 395 400
 290 Leu Val Val Asp Lys Lys Gln Pro Ala Asn His Ala Asp Ala Asn Lys
 291 405 410 415
 294 Ala Gln Ala Leu Pro Glu Thr Gly Glu Asn Pro Phe Ile Gly Thr
 295 420 425 430
 298 Thr Val Phe Gly Gly Leu Ser Leu Ala Leu Gly Ala Ala Leu Leu Ala
 299 435 440 445
 302 Gly Arg Arg Arg Glu Leu
 303 450
 306 <210> SEQ ID NO: 3
 307 <211> LENGTH: 719
 308 <212> TYPE: PRT
 309 <213> ORGANISM: *Peptostreptococcus magnus*
 311 <400> SEQUENCE: 3
 313 Met Ala Ala Leu Ala Gly Ala Ile Val Val Thr Gly Gly Val Gly Ser
 314 1 5 10 15
 317 Tyr Ala Ala Asp Glu Pro Ile Asp Leu Glu Lys Leu Glu Glu Lys Arg
 318 20 25 30
 321 Asp Lys Glu Asn Val Gly Asn Leu Pro Lys Phe Asp Asn Glu Val Lys
 322 35 40 45
 325 Asp Gly Ser Glu Asn Pro Met Ala Lys Tyr Pro Asp Phe Asp Asp Glu
 326 50 55 60
 329 Ala Ser Thr Arg Phe Glu Thr Glu Asn Asn Glu Phe Glu Glu Lys Lys
 330 65 70 75 80
 333 Val Val Ser Asp Asn Phe Phe Asp Gln Ser Glu His Pro Phe Val Glu
 334 85 90 95
 337 Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser Glu Glu Glu
 338 100 105 110
 341 Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser Thr Gln Thr
 342 115 120 125
 345 Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu Ala Tyr Ala
 346 130 135 140
 349 Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val
 350 145 150 155 160
 353 Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys
 354 165 170 175
 357 Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile
 358 180 185 190
 361 Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu
 362 195 200 205
 365 Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu Lys Lys Asp
 366 210 215 220

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369 Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn
 370 225 230 235 240
 373 Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu
 374 245 250 255
 377 Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr
 378 260 265 270
 381 Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg
 382 275 280 285
 385 Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr Val Asp Val
 386 290 295 300
 389 Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys
 390 305 310 315 320
 393 Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile
 394 325 330 335
 397 Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Ala
 398 340 345 350
 401 Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu
 402 355 360 365
 405 Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr Thr Ile Asn
 406 370 375 380
 409 Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu Glu Lys Glu
 410 385 390 395 400
 413 Gln Val Thr Ile Lys Glu Asn Ile Tyr Phe Glu Asp Gly Thr Val Gln
 414 405 410 415
 417 Thr Ala Thr Phe Lys Gly Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr
 418 420 425 430
 421 Arg Tyr Ala Asp Leu Leu Ser Lys Glu His Gly Lys Tyr Thr Ala Asp
 422 435 440 445
 425 Leu Glu Asp Gly Gly Tyr Thr Ile Asn Ile Arg Phe Ala Gly Lys Glu
 426 450 455 460
 429 Glu Pro Glu Glu Thr Pro Glu Lys Pro Glu Val Gln Asp Gly Tyr Ala
 430 465 470 475 480
 433 Ser Tyr Glu Glu Ala Glu Ala Ala Lys Glu Ala Leu Lys Asn Asp
 434 485 490 495
 437 Asp Val Asn Lys Ser Tyr Thr Ile Arg Gln Gly Ala Asp Gly Arg Tyr
 438 500 505 510
 441 Tyr Tyr Val Leu Ser Pro Val Glu Ala Glu Glu Lys Pro Glu Ala
 442 515 520 525
 445 Gln Asn Gly Tyr Ala Thr Tyr Glu Glu Ala Glu Ala Ala Lys Lys
 446 530 535 540
 449 Ala Leu Glu Asn Asp Pro Ile Asn Lys Ser Tyr Ser Ile Arg Gln Gly
 450 545 550 555 560
 453 Ala Asp Gly Arg Tyr Tyr Tyr Val Leu Ser Pro Val Glu Ala Glu Thr
 454 565 570 575
 457 Pro Glu Lys Pro Val Glu Pro Ser Glu Pro Ser Thr Pro Asp Val Pro
 458 580 585 590
 461 Ser Asn Pro Ser Asn Pro Ser Thr Pro Asp Val Pro Ser Thr Pro Asp
 462 595 600 605
 465 Val Pro Ser Asn Pro Ser Thr Pro Glu Val Pro Ser Asn Pro Ser Thr

RAW SEQUENCE LISTING ERROR SUMMARY
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:5

VERIFICATION SUMMARY
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Output Set: N:\CRF4\03062007\J562132.raw

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date